

GenCore version 5.1.5
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 OM nucleic - nucleic search, using sw model
 Run on: May 15, 2003, 02:40:04 ; Search time 4460 Seconds
 (without alignments)
 13163.372 Million cell updates/sec

Title: Perfect score: US-09-804-472-1
 Sequence: 1. gaaaccaggttgttcaggca.....aaaaaaaaaaaaaaaaaa 3625
 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0
 Searched: 16154066 seqs, 809743376 residues

Total number of hits satisfying chosen parameters: 32308132
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%

Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_esthun:*

3: em.estin:*

4: em.estmu:*

5: em.estov:*

6: em.estpl:*

7: em.estro:*

8: em.htc:*

9: gb.est1:*

10: gb.est2:*

11: gb.htc:*

12: gb.est3:*

13: gb.est4:*

14: gb.est5:*

15: em.estfun:*

16: em.estom:*

17: gb.gss:*

18: em.gss_hum:*

19: em.gss_inv:*

20: em.gss_pln:*

21: em.gss_vrt:*

22: em.gss_fun:*

23: em.gss_mam:*

24: em.gss_mus:*

25: em.gss_other:*

26: em.gss_pro:*

27: em.gss_lod:*

SUMMARIES

RESULT 1
 AL521597
 LOCUS AL521597 LTL_NFL004_NBC2 881 bp mRNA linear EST 13-FEB-2001
 DEFINITION prime, mRNA sequence.
 ACCESSION AL521597
 VERSION AL521597.1 GI:12785090
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1. (bases 1 to 881)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Séquençage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cnrs.fr, Web : www.genoscope.cnrs.fr.

FEATURES Source
 1. . 881
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CSDB003YD01"
 /clone_1bb="LTL_NFL004_NBC2"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DR10B"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/note="Organ: brain; vector: pcmsport 6; 1st strand cdna was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cdna was digested with Not I and cloned into the Not I and Eco RV sites of the pcmsport 6 vector. Library was normalized. Library was constructed by life technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>" 1 others

BASE COUNT

271 a 183 c 211 g 215 t

ORIGIN

Query Match 23.9%; Score 868; DB 9; Length 881; Best Local Similarity 99.7%; Pred. No. 9.1e-97; Matches 879; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY

2074 CCTCTAGCTGCTCAGACAGGACATATGACAGTGGATATGAAACATGTTATG 2133

Db

1 CCTCTAGCTGCTCAGACAGGACATATGACAGTGGATATGAAACATGTTATG 60

QY

2134 AAACCAAGTACAGTGGATCTGGGGTGTGTTGCACAGCACACCCATOTCTCCAGAGAAC 2193

Db

61 AAACCAAGTACAGTGGATCTGGGGTGTGTTGCACAGCACACCCATOTCTCCAGAGAAC 120

QY

2194 TTGCCCTCAGAGAGACCTGACAAATGCAATGAGAAGTGCAGGAAACAGAGTA 2253

Db

121 TTGCCCTCAGAGAGACCTGACAAATGCAATGAGAAGTGCAGGAAACAGAGTA 180

QY

2254 TCGTGGGAGTTCTGGGTGTGTTGCACAGCACACCCATOTCTCCAGAGAAC 2313

Db

181 TCGTGGGAGTTCTGGGTGTGTTGCACAGCACACCCATOTCTCCAGAGAAC 240

QY

2314 CTCGCCATTGAACTCTGGCTTACAGTACAGCACACCCATOTCTCCAGAGAAC 2313

Db

241 CTCGCCATTGAACTCTGGCTTACAGTACAGCACACCCATOTCTCCAGAGAAC 300

QY

2374 CCCCAATGGAGATGTGGGATATTCTCGAAAGCCTGGACTGAGCAGTGCTGTTGTA 2433

Db

301 CCCCAATGGAGATGTGGGATATTCTCGAAAGCCTGGACTGAGCAGTGCTGTTGTA 360

QY

2434 CTACACATTGGGCCCTCTTGGCATTTAACAAAAAAAGATATCTCTCGGCCATATGCC 2493

Db

361 CTACACATTGGGCCCTCTTGGCATTTAACAAAAAAAGATATCTCTCGGCCATATGCC 420

QY

2494 AGCGGCACACAGACCCGCCTCAATTATGTAACATGAACTGATCTCACAGATGGAG 253

Db

421 AGCGGCACACAGACCCGCCTCAATTATGTAACATGAACTGATCTCACAGATGGAG 480

QY

2554 AGAGAAACGGAAGAGGAGTTATTGTTGAAATGACAACTCTTAAACCTGAGGGAT 2613

Db

481 AGAGAAACGGAAGAGGAGTTATTGTTGAAATGACAACTCTTAAACCTGAGGGAT 540

QY

2614 CTCCTACTTTTCTCTCTTACAAAAAAAGAAAGAAATATAAGCCGGTTTG 2673

Db

541 CTCCTACTTTTCTCTCTTACAAAAAAAGAAAGAAATATAAGCCGGTTTG 599

QY

2674 CAACATGTTGAAATAATGCTGGATGGGGAGTTGGGAGGATCATACACCATGGTACCT 2733

Db

600 CAACATGTTGAAATAATGCTGGATGGGGAGTTGGGAGGATCATACACCATGGTACCT 659

QY

2734 GAGAGAGGAGAGGAGTGGATTCTCCGCTAACAGAACAGCGGTATCACCTAATG 2793

Db

650 GAGAGAGGAGAGGAGTGGATTCTCCGCTAACAGAACAGCGGTATCACCTAATG 719

QY

2794 TTCTGCACTGGATCATCGCTGGATGGGGAGTTGGGAGGATCATACACCATGGTACCT 2853

Db

720 TTCTGCACTGGATCATCGCTGGATGGGGAGTTGGGAGGATCATACACCATGGTACCT 779

QY

2854 GAGATGAGCAGAGTCTGAGCACCCTGGCTGTGCTCCACATGCAAGACATT 2913

Db

780 GAGATGAGCAGAGTCTGAGCACCCTGGCTGTGCTCCACATGCAAGACATT 839

QY 2914 ATCAGTCCTATTCTAGGGATTACTTGAATTGACCAT 2955
 /note="Organ: brain; vector: pcmsport 6; 1st strand cdna was primed with a NotI-oligo(dt) primer. Five prime end enriched, double-stranded cdna was digested with Not I and cloned into the Not I and Eco RV sites of the pcmsport 6 vector. Library was normalized. Library was constructed by life technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com>" 1 others

RESULT 2

AU133286

DEFINITION

AU133286 NT2RP4

Homo sapiens

cdna

clone

NT2RP4001717

5', mRNA

EST

01-AUG-2002

LOCUS

AU133286

sequence.

ACCESSION

AU133286.1

GI:10993825

VERSION

EST

human.

sapiens

organism

SOURCE

Homo sapiens

REFERENCE

1

(bases 1 to 865)

COMMENT

human

CONTACT

Takao Isogai

GENOMICS

Laboratory

TITLE

HRI human cdna project

(Ota,T., Sugiyama,T., Nishikawa,T., Nakamura,Y., Nagai,T., Sugano,S., Masuho,Y., Isogai,T.)

Unpublished

(2000)

FAX:

81-438-52-3986

EMAIL:

genomics@hri.co.jp

TEL:

81-438-52-3975

HELIX

RESEARCH

INSTITUTE

CDNA LIBRARY

CONSTRUCTION

DEPARTMENT OF

VIROLOGY

INSTITUTE OF MEDICAL SCIENCE

UNIVERSITY OF TOKYO, AND

HELIX

RESEARCH

INSTITUTE

LOCATION/QUALIFIERS

1. .865

ORGANISM

Homo sapiens

/OBJ_XREF

txon:6006

/clone

"NT2RP4001717"

/clone_1

"NT2RP4"

/cell_type

"teratocarcinoma"

/note="vector: pME18S/L3; mRNA from NT2 neuronal precursor

cells after 2-weeks retinoic acid (RA) induction"

BASE COUNT

197 a

173 c

212 g

279 t

4 others

ORIGIN

Query Match

22.1%

Score

800

6;

DB

9;

Length

865;

Best Local Similarity

98.0%

Pred No.

1.4e-88;

Matches

850;

Conservative

0;

Mismatches

13;

Indels

4;

Gaps

4;

Query

1121

TTATGGAGATCATCTT

TTGCTGCTT

TTGCTGCTT</div

RESULT 4	
LOCUS	BM80547
DEFINITION	AGENCOURT [®] 6542949 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5548890
ACCESSION	5', mRNA sequence.
VERSION	BM06547.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1091)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsbs-r@mail.nih.gov
FEATURES	<p>Tissue Procurement: ATCC/DCTD/DTP</p> <p>cDNA Library Preparation: Life Technologies, Inc.</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Agencourt Bioscience Corporation</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>Plate: LLAM1258 row: 1 column: 19</p> <p>High quality sequence stop: 514.</p> <p>Location/Qualifiers</p> <ol style="list-style-type: none"> 1..1091 <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:5548890"</p> <p>/clone_id="NIH_MGC_72"</p> <p>/tissue_type="melanotic melanoma"</p> <p>/lab_host="DH10B (phage resistant)"</p> <p>/note="Organ: skin; Vector: pMW-SHORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."</p>
BASE COUNT	307 a 323 c 265 g 283 t 4 others
ORIGIN	
Query Match	20.7%; Score 750.4; DB 14; Length 1091;
Best Local Similarity	94.4%; Pred. No. 1..5e-82;
Matches	853; Conservative 0; Mismatches 40; Indels 11; Gaps 7;
QY	1484 TTCTCTTGACTACAGAATGAGATGATGCCAGTAATGTGATGACATTCTGA 1543
Db	1 TTCTCTTGACTACAGAATGAGATGATGCCAGTAATGTGATGACATTCTGA 60
QY	1544 TCGTCAGCAGGATGGAGATATTCAGGATATGGCACTATGCTGCACTATATT 1603
Db	61 TCGTCAGCAGGATGGAGATATTCAGGATATGGCACTATGCTGCACTATATT 120
QY	1604 TAAATCATATAGACAGTACTTCAGTTCAGGTTCATGGCTGTTCATCCC 1663
Db	121 TAAATCATATAGACAGTACTTCAGTTCATGGCTGTTCATCCC 180
QY	1664 CAGCATGGCCATTGGAGGATCGCAGGAAGATGGGGATTGGCTGAGGCTGTC 1723
Db	181 CAGCATGGCCATTGGAGGATCGCAGGAAGATGGGGATTGGCTGAGGCTGTC 240
QY	1724 CTACTATCACACGACTGGTTATCTTAAGGAGTGGTGTGAGGCTGGAATATGTC 1783
Db	241 CTACTATCACACGACTGGTTATCTTAAGGAGTGGTGTGAGGCTGGAATATGTC 300
FEATURES	<p>Location/Qualifiers</p> <ol style="list-style-type: none"> 1..1154 <p>/organism="Homo sapiens"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="IMAGE:550896"</p> <p>/clone_id="NIH_MGC_71"</p> <p>/tissue_type="leiomysarcoma"</p>
RESULT 5	
LOCUS	BN542722
DEFINITION	AGENCOURT [®] 5448938 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:550896
ACCESSION	5', mRNA sequence.
VERSION	BN542722
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1154)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgsbs-r@mail.nih.gov
FEATURES	<p>Tissue Procurement: ATCC</p> <p>cDNA Library Preparation: Life Technologies, Inc.</p> <p>cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)</p> <p>DNA Sequencing by: Agencourt Bioscience Corporation</p> <p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov</p> <p>Plate: LLAM12185 row: k column: 09</p> <p>High quality sequence stop: 616.</p> <p>Location/Qualifiers</p> <ol style="list-style-type: none"> 1..1154
BASE COUNT	361 CACC 903
ORIGIN	
Query Match	20.7%; Score 750.4; DB 14; Length 1154;
Best Local Similarity	94.4%; Pred. No. 1..5e-82;
Matches	853; Conservative 0; Mismatches 40; Indels 11; Gaps 7;
QY	1904 CCTTATGGCTCAGTCATGCCAGTAATGGCTGAGATGCCCTGGCGAGGAT 1963
Db	421 CCTTATGGCTCAGTCATGCCAGTAATGGCTGAGATGCCCTGGCGAGGAT 480
QY	1964 TTATGAGACACATCCGATTAATGGATACCCCTCTGGATGAGAAAGAATTCAC 2023
Db	481 TTATGAGACACATCCGATTAATGGATACCCCTCTGGATGAGAAAGAATTCAC 540
QY	2024 TCATACACCTGGCTGAGACGTTATGGATACCCCTCTGGATGAGAAAGAATTCAC 2083
Db	541 TCATACACCTGGCTGAGACGTTATGGATACCCCTCTGGATGAGAAAGAATTCAC 600
Db	661 CAATGAGATTCCTGTCATATGTCAAAG-ATCTCAGAGATTAGTGGATGATGCCCTC 719
QY	2202 AGAGAGACCTGACATGGCAATAG-AAGTGCAGGAAACAGAGAAGTATGCTGG 2260
Db	720 AGAGAGGACTGACATGGCAATAGAAGAAGTGGCAGGAAACAGAGAAGTCTGG 779
Db	7261 CAGTCTCGGGT-GTGTGTTGACGACACCCCATCTCTCCACG-AGAAAGTCTGG 2318
Db	780 CAAGCTCTGGGGTTGCAAGAAGAACCCGATTTCTTACAGCAAGAAGTCTGG 839
QY	2319 CCATGAA--GCTTGACCATTC--GACATGAGCCTTTAACGTGACACACACA 2373
Db	840 CCAATGAAAGCCTTCAAGCAATCTTGAATGAGGCCCTTTACAGTGAACGACCCA 899
QY	2374 CCCC 2377
Db	900 CACC 903

QY 1935 GRGGAGATGCCCTGGCAGGAAAGCATTATGANGCACACATCCGATAATGGTAC 1994
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 700 GRGGTGATGCCCTGGTAGGAGGTTATTGAGAACACATCGACTAAATGGGTAC 641
 QY 1995 CCTCTCTGATGCCAAAGAGAATCTACTCATCCACCCCTGGCTGCTGACGGTATGAGA 2054
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 640 CCTCTCTGATGCCAAAGAGAATCTACTCATCCACCCCTGGCTGCTGACGGTATGAGA 581
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 QY 2055 CCTCGAAGGAATGATCCCTCCCTAGCAGTCCTGACAGAGCAATATGACAGTGAGT 2114
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 580 CCTCGAAGGAATGACCCCTCCCTAGCAGTCCTGACAGAGCAATATGACAGTGAGT 521
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="Taxon:9606"
 /clone="HEMBA106412"
 /clone.lib="HEMBA1"
 /tissue.type="whole embryo, mainly head"
 /dev_stage="embryo, 10 weeks"
 /note="Vector: pME18SFL3"
 /

BASE COUNT
 Query Match
 Best local Similarity 98.1%; Score 697.6; DB 9; Length 830;
 Matches 706; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
 Db 1 CACATGGAAATGACAAACTTGTATGAGCTGCTGCTGAGATGCTACTAACAC 401
 QY 2235 AGGAAGAACAAAGAGGTTATCGCTGGAGTTCTGGGTTGTTGACAGACCCCA 2294
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 400 AGAAAAACAGAGAGGATGTTGGCAGTCCTGGGTTGTTGACAGCATACTCCA 341
 QY 2295 TCTCTTCCAGCAGAAAGTCTGGCTTGAGCTGACATCTGTACATGAGGCC 2354
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 340 TCTCTTCCAGCAGAAAGTCTGGCTTGAGCTGACATCTGTACATGAGGCC 281
 QY 2355 TTACAGTGACAGACCAACCCCATGGAGTTGGTTGATATTTCGAAAGCTGGA 2414
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 280 TTACAGTGACAGACCAACCCCATGGAGTTGGTTGATATTTCGAAAGCTGGA 221
 QY 2415 CTGAGGAGTGTGCTGTACTACAAATGGGCCCTCTGGATATAACAAAGAT 2474
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 220 CTGAGGAGTGTGCTGTACTACAAACGGACCCCTCTGGATATAACAAAGAT 161
 QY 2475 ATCTCTGGCATATGGCCAGAGCIAACCAAGACCCGCTCAATAATGTCAGTGA 2534
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 160 ATCTCTGGCATATGGCCAGAGCIAACCAAGACCCGCTCAATAATGTCAGTGA 101
 QY 2535 ATCTCAGATGAGGAGAGAGAGAGAACGGAGGAGGAGTTATGTTGATAGCACAA 2594
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 100 GTCCTGTAGATGAGGAGGAAACAGAAGAGGAAGGTTGTTGATAGCACAA 41
 QY 2595 CTCTTAACTGAGGGACTCATCTACTTTTTCT 2631
 I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I|||||I
 Db 40 TTCTTAACTGAGGGACTCGGCCACTTTTCT 4

RESULT 7
 AU119689 AU119689 830 bp mRNA linear EST 01-AUG-2002
 LOCUS AU119689 HEMBA1 Homo sapiens clone HEMBA106412 5', mRNA
 DEFINITION sequence.
 ACCESSION AU119689
 VERSION AU119689.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 830)
 AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nawa,T., Sugano,S. and Isobe,T.
 TITLE HRI human cDNA project
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takaaki Isobe
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986

RESULT 8
 AW009467/C LOCUS AW009467
 740 bp mRNA linear EST 08-MAR-2000

DEFINITION	ws83006.x1 NCI CGAP_C03 Homo sapiens cDNA clone IMAGE-2504531 3'	Db	441	CTCAGAGAGACCTGACATTCGAATAGAACAGAAGTGCAGGAAACAGAAGTATCGTT		382
SIMILARITY	similar to SW:CLC3_MOUSE_P51791 CHLORIDE CHANNEL PROTEIN 3 ; , mRNA sequence.					
ACCESSION	AW009467	Qy	2259	GGAGTCTCGGGTGTGTTGACAGCACCCATCTTCCAGAGAAAGTCCCTGG		2318
VERSION	AW009467.1	Qy	381	GGCAGTCTCGGGTGTGTTGACAGCACCCATCTTCCAGAGAAAGTCCCTGG		322
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
BIOLOGICAL_ASSEMBLY	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
MAMMALIA	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 740)	Db	321	CCATGAGCTTCGAGCATCTTGACATGAGCTGAGCACACCCCA		262
AUTHORS		Qy	2379	ATGGAGATGTGGATATTTCGGAAGCAGGGACTGAGCAGTGCACACCCCA		2438
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index					
JOURNAL	Unpublished (1997)	Db	261	ATGGAGATGTGGATATTTCGGAAGCAGTGAGCAGTGCACACCCCA		202
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps_r@mail.nih.gov	Qy	2439	ATGGGCCCTCTGGATATACAAAGATAATCCCGGCATATGGCCGAGC		2498
TISSUE	Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.					
PH.D.		Db	201	ATGGGGCTCTGGATATACAAAGATAATCCCGGCATATGGCCGAGC		142
CDNA LIBRARY PREPARATION	M. Bento Soares, Ph.D.	Qy	2499	GCRAACAAAGACCCGCCTCATAATGTCACACTGAATCAGAGAGAG		2558
CDNA LIBRARY ARRAYING	Greg Lennon, Ph.D.	Db	141	GCRAACAAAGACCCGCCTCATAATGTCACACTGAATCAGAGAGAG		82
CDNA SEQUENCING	Washington University Genome Sequencing Center	Qy	2559	AAACGGAGAGGAGTGTATTAGTGTAGAACACTTAACTGAGGAGTCCT		2618
CLONE DISTRIBUTION	NCI-CGAP clone distribution information can be found through the T.M.A.G.E. Consortium/LINL at: www.bio.llnl.gov/biopr/image/image.html	Db	81	AAACGGAGAGGAGTGTATTAGTGTAGAACACTTAACTGAGGAGTCCT		22
INSERT LENGTH	400	Std Error: 0.00				
SEQ PRIMER	-40UP from Gibco	Qy	2619	ACTTTTTCTCTTTACAA		
HIGH QUALITY SEQUENCE	sequence stop: 449.					
FEATURES	Location/Qualifiers					
SOURCE	1. -740					
/organism="Homo sapiens"						
/db_xref="taxon:9605"						
/clone_1lib="NCI-CGAP_C03"						
/sex="pooled"						
/tissue_type="colon"						
/lab_host="DH10B"						
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was prepared from 12 pooled bulk tumor samples and primed with a Not I - oligo(dt) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization."						
BASE COUNT	181 a 164 c 172 g 222 t 1 others					
ORIGIN						
QUERY MATCH	19.2%; Score 696; DB 10; Length 740;					
BEST LOCAL SIMILARITY	97.0%					
MATCHES	71;					
CONSERVATIVE	0;					
MISMATCHES	21;					
INDELS	1;					
GAPS	1;					
FEATURES	Source					
RESULT	9					
DEFINITION	AU127528					
LOCUS	AU127528 NT2RP2 Homo sapiens	735 bp	mRNA	linear	EST 01-AUG-2002	
DEFINITION	AU127528 NT2RP2 Homo sapiens cDNA clone NT2RP2001481 5', mRNA sequence.					
ACCESSION	AU127528					
VERSION	AU127528.1	Qy	1092244			
KEYWORDS	EST.					
SOURCE	human.					
ORGANISM	Homo sapiens					
BIOLOGICAL_ASSEMBLY	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 735)					
AUTHORS	Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.					
TITLE	HR1 human cDNA project					
JOURNAL	Unpublished (2000)					
COMMENT	Contact: Takao Isogai					
GENOMICS	Genomics Laboratory					
INSTITUTION	Helix Research Institute					
ADDRESS	1532-3 Yana, Kisarazu, Chiba 292-0812, Japan					
TELEPHONE	Tel: 81-438-52-3985					
FAX	Fax: 81-438-52-3985					
EMAIL	genomics@hr1.co.jp					
HR1 HUMAN CDNA PROJECT	5' - & 3' - end one pass sequencing: Helix Research Institute, cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.					
LOCATION/QUALIFIERS	Location/Qualifiers					
FEATURES	Source					
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/cell_type="teratocarcinoma"						
/cell_line="NT2"						
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"						
BASE COUNT	174 a 148 c 172 g 229 t 12 others					
ORIGIN						

JOURNAL		Unpublished (1999)			
Best Local Similarity	95.8%	Score	660.6; DB 9; Length 735;		
Matches	704; Conservative 0; Mismatches 26; Indels 5; Gaps 3;	COMMENT			
DEFINITION	1 GTRWCCTTATTCCTCTAGGGTATTGGAGGCTTGGGACCCCTTTCTATTAGGC	Contact:	Robert Strainsberg, Ph.D.		
REFERENCE	1307 AATATTGGCTGGCTCGACCAAGTCCACCAATTGGAAGTATCCCTCTGG	Email:	cgabps-r@mail.nih.gov		
AUTHORS	61 AAATATTGGCTGGCTCGACCAAGTCCACCAATTGGAAGTATCCCTCTGG	Tissue Procurement:	The Cepko Laboratory		
KEYWORDS	b b	CDNA Library Preparation:	Life Technologies, Inc.		
SOURCE	b b	CDNA Library Arrayed by:	The T.M.A.G.E. Consortium (LNU)		
ORGANISM	Mus musculus	DNA Sequencing by:	Agencourt Bioscience Corporation		
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mus musculus	Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNU at: http://image.llnl.gov	Clone distribution:	MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LNU at: http://image.llnl.gov		
RESULTS	10	http://image.llnl.gov			
OCUS	B0960629	Plate:	LLAM3996		
DEFINITION	891 bp mRNA	row: 0	row: 21		
CCSSION	NIH_MGC_94	column: 21			
ERTION	Mus musculus	High quality sequence stop:	671.		
EWORDS		Location/Qualifiers			
EST.		1. . 891			
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		/lab_host="DH10B (phage-resistant)"			
		/note="Organ: eye; Vector: PCMV-SPORE; site_1: NotI; site_2: Sall; cloned unidirectionally; oligo-dr primed. Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.			
		Note: this is a NH_MGC Library."			
BASE COUNT	278	a	183 c		
ORIGIN		209 g	218 t		
		3 others			
Query Match	18.2%	Score	660.6; DB 14; Length 891;		
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Matches	757; Conservative 0; Mismatches 117; Indels 8; Gaps 2;	Matches	757; Conservative 0; Mismatches 117; Indels 8; Gaps 2;		
DEFINITION	1607 AATCTATAATGACAGTATTCTTGGATCAGTCAGGTTCCATCAGCTTGCTTCACTATTTA	QY	1920 ATGACCGATAATGGTGGAGATGCGCTTGGCAGGGAGGCAATTAGAACACATTC		
REFERENCE	301 TCCAGCAGGCCATTGGATATTCAGCTATGGCAGTATGGCTGGACTCATTTA	Db	1667 CATGCCATGAGCCATGCGAGGATTGGGGATTCGGGGAGCCTTGCTTA		
AUTHORS	b b	2	1726 CATGCCATGAGCCATGCGAGGATTGGGGATTCGGGGAGCANCNTGCTTA		
KEYWORDS	b	421 CATGCCATGAGCCATGCGAGGATTGGGGATTCGGGGAGCANCNTGCTTA	QY	1980 CGATTAATGATGACCCCTTCTGGATGCGAAAGAGGATTCTACTCACACACCTGCT	
SOURCE	b	481 CTATCACCAGCAGCTGGTTATCTTAAGAATGGTGTNAGGTCNCGGGTGATTCATAC	Db	1727 CTATCACCAGCAGCTGGTTATCTTAAGAATGGTGTNAGGTCNCGGGTGATTCATAC	
ORGANISM	b	540 1787 ACCTGGCCCTTATGCCATGGTSGTGTGATGCTGAGTGGTGTG-TGACAGAATG	QY	1786 1787 ACCTGGCCCTTATGCCATGGTSGTGTGATGCTGAGTGGTGTG-TGACAGAATG	
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mus musculus	600	541 ACCTGGCCCTTATGCCATGGTSGTGTGATGCTGAGTGGTGTG-TGACAGAATG	Db	1845 CTGCTCTCTGCTGTTATGGCTTACTGGGGCTT-GGAATATATGTTGCC	
RESULTS	10	600	601 CTGCTCTCTGCTGTTATGGCTTACTGGGGCTT-GGAATATATGTTGCC	QY	1905 CTTATGGCTGCAGCTGATGCCAGAAATGGTGGAGATGCCCTT-GGCAGGAAAGC
OCUS	B0960629	600	661 CTTATGGCTGCAGCTGATGCCAGAAATGGTGGAGATGCCCTT-GGCAGGAAAGC	Db	1961 1961 CTTATGGCTGCAGCTGATGCCAGAAATGGTGGAGATGCCCTT-GGCAGGAAAGC
DEFINITION	891 bp mRNA	720	720	QY	2220 GCAATAGAAGTGGCAGGAAAAACAGAAGGATTCAGAGTGGGGATGGCTCAGAGGACCTGACATT
REFERENCE	NIH_MGC_94	Db	721 ATTATGAAAGCACAC 1976	Db	2279 GCAATAGAAGTGGCAGGAAAAACAGAAGGATTCAGAGTGGGGATGGCTCAGAGGACCTGACATT
AUTHORS	Mus musculus	721 ATTATGAAAGCACAC 735	QY	302 GCAATAGAAGTGGCAGGAAAAACAGAAGGATTCAGAGTGGGGATGGCTCAGAGGACCTGACATT	
KEYWORDS			QY	328 GCAATAGAAGTGGCAGGAAAAACAGAAGGATTCAGAGTGGGGATGGCTCAGAGGACCTGACATT	
SOURCE			Db	362 GCAATAGAAGTGGCAGGAAAAACAGAAGGATTCAGAGTGGGGATGGCTCAGAGGACCTGACATT	
ORGANISM	Mus musculus		QY	362 GCAATAGAAGTGGCAGGAAAAACAGAAGGATTCAGAGTGGGGATGGCTCAGAGGACCTGACATT	
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mus musculus			Db	423 CTTCGAAACTGGGACTTACAGTCAGACAGACCCACCCATGGAGATGGTGTGATTT	
RESULTS	10		QY	2399 423 CTTCGAAACTGGGACTTACAGTCAGACAGACCCACCCATGGAGATGGTGTGATTT	
OCUS	B0960629		Db	422 CTTCGAAACTGGGACTTACAGTCAGACAGACCCACCCATGGAGATGGTGTGATTT	
DEFINITION	891 bp mRNA		QY	2400 TTCCGAAACTGGGACTTACAGTCAGACAGACCCACCCATGGAGATGGTGTGATTT	
REFERENCE	NIH_MGC_94		Db	2459 TTCCGAAACTGGGACTTACAGTCAGACAGACCCACCCATGGAGATGGTGTGATTT	
AUTHORS	Mus musculus		Db	482 TTTCGAAACTGGGACTTACAGTCAGACAGACCCACCCATGGAGATGGTGTGATTT	
KEYWORDS			QY	2460 ATAACAAAAGATATCTCCGGCATGGCCAGACGGAAACCAAGACCCGCTCA	
SOURCE			QY	2519 ATAACAAAAGATATCTCCGGCATGGCCAGACGGAAACCAAGACCCGCTCA	
ORGANISM	Mus musculus		Db	542 ATAACAAAAGATATCTCCGGCATGGCCAGACGGAAACCAAGACCCGCTCA	
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mus musculus			QY	601 ATAACAAAAGATATCTCCGGCATGGCCAGACGGAAACCAAGACCCGCTCA	
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KEYWORDS					
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AUTHORS	Mus musculus				
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EUKARYOTA					

QY	3310	GCGGAGAACGAAATCCTCTCATGTTGTCGCCGTCGTCCTGACAGGACATGAGCTG	3369
Db	430	GCGAGAACGAAATCCTCTCATGTTGTCGCCGTCGTCCTGACAGGACATGAGCTG	371
OY	3370	GTTTAAAGGATAAAGTTKTTTGTTCCTCTCAGACTTATGGATAATGTGACC	3429
Db	370	GTTTAAAGGATAAAGTTKTTTGTTCCTCTCAGACTTATGGATAATGTGACC	311
QY	3430	GGGTCTATGCAATTTCATGAAACTACTATGATATAAGTGCTGTTGAG	3489
Db	310	GGGTCTATGCAATTTCATGAAACTACTATGATATAAGTGCTGTTGAG	251
OY	3490	CATAATTAATAATGCTCTGCTTGAGTAAGAGAAAAA	3534
Db	250	CATAATTAATAATGCTCTGCTTGAGTAAGAGAAAAA	206
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DEFINITION	At889196	linear	EST
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AUTHORS		3	
TITLE	Similar to SW:CLC3_MOUSE P51791 CHLORIDE CHANNEL PROTEIN	3	, mRNA
JOURNAL			
COMMENT			
FEATURES			
source			
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
1 (bases 1 to 684)			
NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.		
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index			
Unpublished (1997)			
Contact: Robert Strausberg, Ph.D.			
Email: cgaps-r@mail.nih.gov			
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R. Emmert-Buck, M.D., Ph.D.			
cDNA Library Preparation: Life Technologies, Inc.			
cDNA Library Arrayed by: Greg Lennon, Ph.D.			
DNA Sequencing by: Washington University Genome Sequencing Center			
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html			
Seq primer: -40UP from Gibco			
High quality sequence stop: 406.			
RESULT 15			
LOCUS	BQ433763	1023 bp	mRNA
DEFINITION	BQ433763	LINEAR	EST
REFERENCE	AGENCOURT_776656	NTH_MGC_68	Homo sapiens cDNA clone IMAGE:6022145
ACCESSION	5'	mRNA	sequence.
VERSION	BQ433763		
COMMENT			
FEATURES			
source			
ORGANISM	Homo sapiens		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.			
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NIH MGC	http://mgc.nci.nih.gov.		
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Robert Strausberg, Ph.D.			
Email: cgaps-r@mail.nih.gov			
Tissue Procurement: DCIP/DRP/Gazdar			
cDNA Library Preparation: Life Technologies, Inc.			
DNA Sequencing by: Agenecourt Bioscience Corporation (LLNL)			
DNA Sequencing by: Agenecourt Bioscience Corporation (LLNL)			
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:			
http://image.llnl.gov			
Plate: LIAM1328	row: p	column: 18	
High quality sequence stop: 514			

FEATURES source	Location/Qualifiers
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/clone="IMAGE:602145"	QY 574 GGTCAACACACGACAGCTGCTGTTGGGATCTATGAAACACATGGAGAGGGATA 633
/clone_id="NIH_MGC_68"	1 GGTACACACACGACAGCTGCTGTTGGGATCTATGAAACACATGGAGAGGGATA 60
/tissue_type="large cell carcinoma"	QY 634 AACGCCACAGTGGAAACATGGGAGATTATCATAGTCAGCAGAGGGCTCTGGT 693
/lab_host="BBL10B (phase-resistant)"	61 AACGCCACAGTGGAAACATGGGAGATTATCATAGTCAGCAGAGGGCTCTGGT 120
Site 2: Salt-Cloned unidirectionally. Primer: Oligo dT.	Db 694 CTTATATCATGAACTACATAATGTCACATCTCTGGCCCTGAGTTGGCTTCTTGCG 753
Average insert size 1.8 kb. Library constructed by Life	Db 121 CTTATATCATGAACTACATAATGTCACATCTCTGGCCCTGAGTTGGCTTCTTGCG 180
Technologies	QY 754 TTRCCCTGGTAAGTATGCTCATATGCCCTGGCATGGATTCCAGAGATAAA 813
ORIGIN	181 TTRCCCTGGTAAGTATGCTCATATGCCCTGGCATGGATTCCAGAGATAAA 240
BASE COUNT	QY 814 CTATTTAAGGGTTCATCATGAGGTTACTTGGAAATGGACTTAATGATAAA 873
270 a 209 c 221 g 319 t 4 others	Db 241 CTATTTAAGGGTTCATCATGAGGTTACTTGGAAATGGACTTAATGATAAA 300
Db 874 CCATCACATTTAGTCCTGGCTGGCATCGGTTGAGTTAGGAAGAGAGGTCCTGG 933	QY 301 CCATCACATTTAGTCCTGGCTGGCATCGGTTGAGTTAGGAAGAGAGGTCCTGG 360
Db 934 TACATGTTGCTGTCGGAAATCTTCTCTACCTCTTCCAAGATATGACAA 993	QY 361 TACATGTTGCTGTCGGAAATATCTTCTACCTCTTCCAAGATATGACAA 420
Db 994 ACGAGCTAAAGAGGGCTCTATGAGCTCCCTCGCTCGAGGSGTTCTGTACCT 1053	QY 421 ACGAGCTAAAGAGGGCTCTATGAGCTCCCTCGCTCGAGGSGTTCTGTACCT 480
Db 1054 TTGGCCACCAATTGGAGGAGTCCTTTAGCCCTGGAGAGGTAGCTATTATTCCTC 1113	QY 481 TTGGCCACCAATTGGAGGAGTCCTTTAGCCCTGGAGAGGTAGCTATTATTCCTC 540
QY 1114 TCAAACATTATGGAGATCATTTTGTGCTGTTAGTGCTGATTTGGTCA 1113	Db 541 TCAAACATTATGGAGATCATTTTGTGCTGTTAGTGCTGATTTGGTCA 600
Db 541 TCAAACATTATGGAGATCATTTTGTGCTGTTAGTGCTGATTTGGTCA 600	QY 1174 TCAATCCATTGACGCCGCTGGCCCTTTATGGAGGTAGCTATTATTCCTC 1230
Db 601 TCAATCCATTGACGCCGCTGGCCCTTTATGGAGGTAGCTATTATTCCTC 660	QY 1231 GGTAACCTTTAACGGTTCCCTTATTCCTCCAGGG 1269
QY 661 GGTAACCTTTAACGGTTCCCTTATTCCTCCAGGG 702	Search completed: May 15, 2003, 06:45:02 Job time : 4496 secs